

Query= SEQ ID NO:1
(618 letters)

Sequences producing significant alignments:

	Score (bits)	E Value
--	-----------------	------------

AC114490.2.1.152428

1222 0.0

>AC114490.2.1.152428
Length = 152428

Score = 1222 bits (616), Expect = 0.0
Identities = 617/618 (99%)
Strand = Plus / Minus

Query: 1 atgggggctgcctttgtcgctagcctccgcagtaacctttcttctgccacttcaagggtca 60
|||||
Sbjct: 107249 atgggggctgcctttgtcgctagcctccgcagtaacctttcttctgccacttcaagggtca 107190

Query: 61 gagatgaacagcagtggtggggacctgggtggtggcggctgcagcctctgggatgaccct 120
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Sbjct: 107189 gagatgaacagcagtggtggggacctgggtggtggcggctgcagcctctgggatgaccct 107130

Query: 121 gctcgcttcacgtggtgcccgcggcctatgccttggcactgggcctggggctgccagcc 180
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Sbjct: 107129 gctcgcttcacgtggtgcccgcggcctatgccttggcactgggcctggggctgccagcc 107070

Query: 181 aacgtggcggccctggcaatgttcacccgcagcggcgggcgccctggggccaggccctgctt 240
|||||
Sbjct: 107069 aacgtggcggccctggcaatgttcacccgcagcggcgggcgccctggggccaggccctgctt 107010

Query: 241 ctctacctgttcaacctggctctggttgatgagttcttcacgctcacgctgcagctgtgg 300
|||||
Sbjct: 107009 ctctacctgttcaacctggctctggttgatgagttcttcacgctcacgctgcagctgtgg 106950

Query: 301 ctcacctactacctgggcctggcccgaggccgcctgccacgcggccggggccacctact 360
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Sbjct: 106949 ctcacctactacctgggcctggcccgaggccgcctgccacgcggccggggccacctact 106890










Query: 361 acgtgtccacctatgcggcggtggtcttcgccgcgctcatcagcgtgtgccgctgcggct 420
|||||
Sbjct: 106889 acgtgtccacctatgcggcggtggtcttcgccgcgctcatcagcgtgtgccgctgcggct 106830

Query: 421 tcgtacgcggtcccggggccaggcggtgccccgctggccccggtgcctacggbgccccg 480
|||||
Sbjct: 106829 tcgtacgcggtcccggggccaggcggtgccccgctggccccggtgcctacggbgccccg 106770

Query: 481 cgcgcgctgectgcgccttcgcctggctggcgggcctggccccctccctgcctggagcacc 540
||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 106769 cgcgcgctgectgcgccttcgcctggctggcgggcctggccccctccctgcctggagcacc 106710

Query: 541 gctgggcaagctcggggctggcctcgcgcacggtggccttcgcggccgccttcctgctgg 600
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Sbjct: 106709 gctgggcaagctcggggctggcctcgcgcacggtggccttcgcggccgccttcctgctgg 106650

Query: 601 tgctcgcgccaacgtga 618
||||||||||||||||
Sbjct: 106649 tgctcgcgccaacgtga 106632

PubMed Nucleotide Protein Genome Structure PMC Taxonomy OMIM Boo

Search for

Limits Preview/Index History Clipboard Details

Display Show:

☐ 1: AC114490. Homo sapiens chro...[gi:20340495]

Links

LOCUS AC114490 152428 bp DNA linear PRI 30-APR-2002
 DEFINITION Homo sapiens chromosome 1 clone RP11-244H3, complete sequence.
 ACCESSION AC114490 AL354876
 VERSION AC114490.2 GI:20340495
 KEYWORDS HTG.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 152428)
 AUTHORS Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Rouse,G., Wu,Z.,
 Saenphimmachak,C., Phelps,K.A., Buckley,D., Raymond,C. and
 Haugen,E.D.
 TITLE Direct Submission
 JOURNAL Unpublished

REFERENCE 2 (bases 1 to 152428)
 AUTHORS Kaul,R.K., Olson,M.V., Raymond,C. and Haugen,E.D.
 TITLE Direct Submission
 JOURNAL Submitted (09-MAR-2002) Genome Center, University of Washington,
 Box 352145, Seattle, WA 98195, USA

REFERENCE 3 (bases 1 to 152428)
 AUTHORS Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Rouse,G., Wu,Z.,
 Saenphimmachak,C., Phelps,K.A., Buckley,D., Raymond,C. and
 Haugen,E.D.
 TITLE Direct Submission
 JOURNAL Submitted (30-APR-2002) Genome Center, University of Washington,
 Box 352145, Seattle, WA 98195, USA

COMMENT On Apr 30, 2002 this sequence version replaced gi:19310309.
 ----- Genome Center
 Center: University of Washington Genome Center
 Center Code: UWGC
 Web site: <http://www.genome.washington.edu>
 Contact: uwgchtgs@u.washington.edu
 Drafting Center: SC

----- Project Information
 Center project name: chr-1
 Center clone name: RP11-244H3 (sc0659)

----- Summary Statistics
 Sequencing vector: plasmid; 31% of reads
 Sequencing vector: plasmid; L08752; 69% of reads
 Chemistry: Dye-terminator ET; 89% of reads
 Chemistry: Dye-terminator Big Dye; 11% of reads
 Assembly program: Phrap; version 0.990319
 Consensus quality: 152402 bases at least Q40
 Consensus quality: 152428 bases at least Q30
 Consensus quality: 152428 bases at least Q20
 Insert size: 152428; sum-of-contigs